

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model
Run on: October 8, 2003, 16:29:18 ; Search time 3342.44 Seconds
(without alignments)
4381.722 Million cell updates/sec

Title: US-10-001-848-3_COPY_18_375
Perfect score: 1894
Sequence: 1 AFPPAAARGPPKMDKVP.....LPDPKPGPPVASSSSATSL 358

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 2888711 seqs, 20454813386 residues
Total number of hits satisfying chosen parameters: 5777422
Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+p2n.model -DEV=xlp
-Q=/cgn2.1/USPTO_epool_p/US10001848/runat_08102003_130420_22053/app_query.fasta_1.1166
-DB=GenEmbl -QPMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTPMT=ptc -NORM=ext -HEADSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US10001848 -CGN 1_4241 @runat_08102003_130420_22053 -NCPU=3
-NO_MMAP -LARGQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:
1: gb_ba:*
2: gb_hcg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_ats:*
12: gb_ay:*
13: gb_un:*
14: gb_vi:*
15: em_ba:*
16: em_fun:*
17: em_hum:*
18: em_in:*
19: em_mu:*
20: em_om:*
21: em_or:*
22: em_ov:*
23: em_pat:*
24: em_ph:*
25: em_pl:*
26: em_ro:*
27: em_ats:*
28: em_un:*

29: em_vi:*
30: em_hcg_hum:*
31: em_hcg_inv:*
32: em_hcg_other:*
33: em_hcg_mus:*
34: em_hcg_pln:*
35: em_hcg_rod:*
36: em_hcg_mam:*
37: em_hcg_vrt:*
38: em_sy:*
39: em_hbgo_hum:*
40: em_hbgo_mus:*
41: em_hbgo_other:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1894	100.0	1450	6	AX287596 Sequence
2	1894	100.0	3305	9	BC036769 Homo sapi
3	1894	100.0	3402	6	AR252460 Sequence
4	1894	100.0	3402	6	AX080803 Sequence
5	1894	100.0	3402	6	AX191426 Sequence
6	1894	100.0	3402	6	AX403231 Sequence
7	1886	99.6	1565	9	AF279689 Homo sapi
8	1886	99.6	3080	6	AX287610 Sequence
9	1886	99.6	3080	9	HS2277437
10	1886	99.6	3112	6	AX287608 Sequence
11	1886	99.6	3397	9	AF312678 Homo sapi
12	1785	94.2	1967	6	AR156834 Sequence
13	1785	94.2	2274	10	MMU2931947
14	1785	94.2	2277	6	AX287593 Sequence
15	1785	94.2	2359	10	AF3213100
16	1767	93.3	1788	6	AX287613 Sequence
17	1566	82.7	1004	6	AR156836 Sequence
18	1468	77.5	177950	9	AC019103 Homo sapi
19	1414.5	74.7	3256	10	AF3213302
20	1410.5	74.5	24181	10	MMU308490
21	1410.5	74.5	165443	2	AC079939 Mus muscu
22	1410.5	74.5	176874	2	AC123743 Mus muscu
23	1402.5	74.0	2274	5	BC053245 Danio rer
24	1402.5	74.0	187234	2	AC117047 Rattus no
25	1402.5	74.0	346077	2	AC106235 Rattus no
26	1364	72.0	2178	6	AX224732 Sequence
27	1356.5	71.6	232203	2	AC127933 Rattus no
28	1290	68.1	2339	10	AF3213301
29	1279.5	67.6	1742	6	AR156835 Sequence
30	1184	61.5	781	6	AX080801 Sequence
31	1154.5	61.0	182635	2	AC140291 Mus muscu
32	861	45.5	493	6	AX318742 Sequence
33	611	32.3	384	6	AR156833 Sequence
34	606	32.0	152648	2	AC122772 Mus muscu
35	524	27.7	148850	2	EX247870 Danio rer
36	524	27.7	204579	2	AL954843 Danio rer
37	492	26.0	3002	5	AF157560 P.waltlii m
38	487	25.7	3468	5	PF6GPR4 U24491 Xenopus lae
39	484.5	25.6	2763	5	XMU24491
40	482.5	25.5	3634	5	PF6GPR3 M55163 Xenopus lae
41	482.5	25.5	3815	5	XELX1FGFR S56291 sam3=FGFR3
42	475.5	25.1	2520	10	S56291 BC053056 Mus muscu
43	475.5	25.1	4156	10	BC053056 M81342 BALB/c fibr
44	475.5	25.1	4158	10	MUSMFR3
45	473.5	25.0	2403	6	AX695736 Sequence

ALIGNMENTS

RESULT 1

QY	121	AppProAlaSerGlnGlnTrpAlaArgProArgPheThrGlnProSerLysMetArgAcg	140
Db	444	GACCCCGCAGCGAGCAGTGGGACACACCGCGCTTCACACAGCCCTCCCAAGATGAGCGCGC	503
QY	141	ArgValIleAlaArgProValGlySerSerValArgLeuLysCysValAlaSerGlyHis	160
Db	504	CGGGTGATCGCAGCGCCCGTGGGTAGCTCCGTGGGCTCAAGTGGCTGGCCAGCGCGCAC	563
QY	161	ProArgProAspIleThrTrpMetLysAspAspGlnAlaLeuThrArgProGluAlaAa	180
Db	564	CCTCGCGCCGACATCAGTGGATGAAGAGCAGACAGCGCTTGACGGCGCCACAGGCGCT	622
QY	181	GluProArgLysLysLysTrpThrLeuSerLeuLysAsnLeuArgProGluAspSerGly	200
Db	624	GAGCCCGAAGAGAGTGGACACTAGCCTGAAGAACTCGCGCGCGAGACGCGGC	688
QY	201	LysTyThrCysArgValSerAsnArgAlaGlyValAlaIleAsnAlaThrTyLysValAsp	220
Db	684	AAATACACCTGCCCGCTGTGCAACCCGCGCGCGCCATCAACGCCCACTACAAAGGTGGAT	743
QY	221	ValIleGlnArgThrArgSerLysProValLeuThrGlyThrHisProValAsnThrThr	240
Db	744	GTGATCCAGCGGACCCGTTCCAAAGCCCGTCTCACAGGACGACCCCGTGAACACGACG	803
QY	241	ValAspPheGlyThrThrSerPheGlnCysLysValArgSerAspValLysProVal	260
Db	804	GTGGACTCTCGGGGGACACCGTCTTCCAGTGCAGGTGCGCAGCGACGCTGAAGCCGGTG	863
QY	261	IleGlnTrpLeuLysArgValGluTyThrGlyValAlaGluGlyArgHisAsnSerThrIleAsp	280
Db	864	ATCCAGTGGCTGAAGCGCGTGGAGTAGTACGGCGCTGAGGGCGCCGACCAACTCCACCATCGAT	923
QY	281	ValGlyGlyGlnLysPheValValLeuProThrGlyAspValTrpSerArgProAspGly	300
Db	924	GTGGGGCGCCAGAGTTTGTGGTGCTGCCACGGGTGACGTGTGTGCGCGCCGACGCGC	983
QY	301	SerTyLeuAsnLysLeuLeuIleThrArgAlaArgGlnAspAspAlaGlyMetTyIle	320
Db	984	TCCTAGCTCAATTAAGCTGCTCATCACCGCTGCCCGCAGCAGACATGCGGCATGTACATC	1043
QY	321	CysLeuGlyAlaLeuThrMetGlyTyThrSerPheArgSerAlaPheLeuThrValLeuPro	340
Db	1044	TGCTTGGCGCCCAACACCATGGGCTCAGCTTCGCGACGCGCTTCTCACCGTGTGCTCCA	1103
QY	341	AspProLysProGlyProProValAlaSerSerSerSerAlaThrSerLeu	358
Db	1104	GACCCAAACCGCCAGGGCCACCTGTGGCTCCTCGTCTCGGCCACTAGCCTG 1:57	
RESULT 2			
LOCUS	BC036769	3305 bp mRNA linear PRI 26-AUG-2002	
DEFINITION	Homo sapiens, clone MGC:46034 IMAGE:5744684, mRNA, complete cds.		
ACCESSION	BC036769		
VERSION	BC036769.1	GI:22477841	
KEYWORDS	MGC.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Mammalia; Primates; Catarrhini; Hominidae; Homo.		
AUTHORS	1 (bases 1 to 3305)		
TITLE	Strausberg, R.		
JOURNAL	Direct Submission		
REMARK	Submitted (23-AUG-2002) National Institutes of Health, Mammalian		
COMMENT	Gene Collection (MGC), Cancer Genomics Office, National Cancer		
	Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,		
	USA		
	NIH-MGC Project URL: http://mgc.nci.nih.gov		
	Contact: MGC help desk		
	Email: cgaps-f@mail.nih.gov		
	Tissue Procurement: Life Technologies, Inc.		
	cDNA Library Preparation: Life Technologies, Inc.		
	DNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)		
	DNA Sequencing by: National Institutes of Health Intramural		

Db 301 QKVVLPDGVMSRPGSVLNLKLLITRARODDAGMYICLGANTMGYSFRSAPLTVLPDPK 360
 Qy 361 PPGPPVASSSSATSLPWPVIGIPAGAVFLLTLLMLCQAQKPCPTAPAPPLPGRPP 420
 Db 361 PPGPPVASSSSATSLPWPVIGIPAGAVFLLTLLMLCQAQKPCPTAPAPPLPGRPP 420
 Qy 421 GTARDSDGKDLPSLAALSAGPGVGLCEHSGSPAPOHLLGPGVAGPKLYPKLYTDIHT 480
 Db 421 GTARDSDGKDLPSLAALSAGPGVGLCEHSGSPAPOHLLGPGVAGPKLYPKLYTDIHT 480
 Qy 481 HTHSHSHSHVHGKVKHQHIHYQC 504
 Db 481 HTHSHSHSHVHGKVKHQHIHYQC 504

RESULT 7

AAU81961
 ID AAU81961 standard; Protein; 504 AA.
 AC AAU81961;
 DT 09-APR-2002 (first entry)
 XX Human PRO943.
 XX Human; PRO; antiinflammatory; ophthalmological; vasotropic;
 KW retinal cell injury; ocular disease; retinitis pigmentosa;
 KW macular degeneration; retinal detachment; retinal tear; retinopathy;
 KW retinal degenerative disease; macular hole; degenerative myopia;
 KW acute retinal necrosis syndrome; traumatic choriorretinopathy;
 KW Purtscher's retinopathy; oedema; ischaemic condition;
 KW retinal vision occlusion; collagen vascular disease;
 KW thrombocytopaenic purpura; uveitis; retinal vasculitis; Bales disease;
 KW systemic lupus erythematosus; environmental trauma.

XX Homo sapiens.

OS WO200109327-A2.

XX 08-FEB-2001.

XX 28-JUL-2000; 2000WO-US20710.

XX 28-JUL-1999; 99US-146222P.

XX 13-SEP-1999; 99WO-US20944.

XX 15-SEP-1999; 99WO-US21090.

XX 29-NOV-1999; 99WO-US28214.

XX 30-NOV-1999; 99WO-US28313.

XX 01-DEC-1999; 99WO-US28301.

XX 05-JAN-2000; 2000WO-US00219.

XX 06-JAN-2000; 2000WO-US00376.

XX 11-FEB-2000; 2000WO-US03565.

XX 18-FEB-2000; 2000WO-US04341.

XX 22-FEB-2000; 2000WO-US04414.

XX 24-FEB-2000; 2000WO-US05004.

XX 02-MAR-2000; 2000WO-US05841.

XX 15-MAR-2000; 2000WO-US06884.

XX 30-MAR-2000; 2000WO-US08439.

XX 17-MAY-2000; 2000WO-US13705.

XX (GETH) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Goddard A, Godowski PJ, Gurney AL;

XX Kljavin IJ, Lafleur M, Mark MR, Marsters SA, Pitti RM;

XX Watanabe CK, Wood WT;

XX WPI; 2002-130120/17.

XX N-PSDB; ABK28591.

XX Promoting survival of retinal cells, or delaying or preventing retinal

XX cell injury or death, by contacting retinal cells with PRO175, 220,

XX 216, 243, 306, 346, 322, 536, 943, 840, 828, 826, 1088 or PRO1132

XX polypeptide -

XX PS
 XX CC
 CC The invention relates to promoting the survival of retinal cells, or
 CC delaying or preventing retinal cell injury or death, by contacting the
 CC retinal cells with the polypeptide such as PRO175, PRO220, PRO216,
 CC PRO243, PRO306, PRO346, PRO322, PRO336, PRO943, PRO840, PRO828, PRO826,
 CC PRO1068 or PRO1132 polypeptide. Also included are the nucleic acids
 CC encoding the PRO proteins, a vector comprising the nucleic acid, a host
 CC cell comprising the vector, and anti-PRO antibody. The PRO proteins are
 CC useful for promoting survival of retinal cells (retinal neurons such as
 CC retinal ganglion cells, displaced retinal ganglion cells, amacrine
 CC cells, displaced amacrine cells, horizontal neurons or bipolar neurons,
 CC rod photoreceptors, or supportive cells such as Muller cells or pigment
 CC epithelial cells), or delaying or preventing retinal cell injury or
 CC death caused by ocular disease (which is or is associated with
 CC retinitis pigmentosa, macular degeneration, retinal detachment, ret
 CC tear, retinopathy, retinal degenerative disease, macular hole,
 CC degenerative myopia, acute retinal necrosis syndrome, traumatic
 CC choriorretinopathy or contusion, Purtscher's retinopathy, oedema, an
 CC ischaemic condition, central or branch retinal vision occlusion,
 CC collagen vascular disease, thrombocytopaenic purpura, uveitis, retinal
 CC vasculitis, occlusion associated with Bales disease or systemic lupus
 CC erythematosus), retinal injury or environmental trauma. The retinal
 CC cell injury or death is delayed or prevented by substantially not
 CC causing angiogenesis or mitogenesis. The present sequence represents
 CC a PRO protein.
 XX SQ

Sequence 504 AA;

Query Match 100.0%; Score 2709; DB 23; Length 504;
 Best Local Similarity 100.0%; Pred. No. 7,3e-164;
 Matches 504; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MTPSPDLLLPPLLGAPPPAAAARGPPKMAKVVPRQVAFRLGRTVRLQCPVEGDPPL 60
 Db 1 MTPSPDLLLPPLLGAPPPAAAARGPPKMAKVVPRQVAFRLGRTVRLQCPVEGDPPL 60
 Qy 61 TWMTXGRTIHSGMSRFRVLPGGLKVKQVEREDAGVYCKATNGFGSLVNYTLVLLDI 120
 Db 61 TWMTXGRTIHSGMSRFRVLPGGLKVKQVEREDAGVYCKATNGFGSLVNYTLVLLDI 120
 Qy 121 SPKESLGPDSGGQEDPPASQOMARPRFTOPSKMRRRVIAARPVGSSVRLKCVASGHRPP 180
 Db 121 SPKESLGPDSGGQEDPPASQOMARPRFTOPSKMRRRVIAARPVGSSVRLKCVASGHRPP 180
 Qy 181 DITMKDDOALTRPEAAAPRKCKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQ 240
 Db 181 DITMKDDOALTRPEAAAPRKCKWTLSLKNLRPEDSGKYTCRVSNRAGAINATYKVDVIQ 240
 Qy 241 RTRSKPVLGTGHPVNTTVDGTTTSFOCKVRSQVDPVQLKRVYEGAGRHNSIDVGG 300
 Db 241 RTRSKPVLGTGHPVNTTVDGTTTSFOCKVRSQVDPVQLKRVYEGAGRHNSIDVGG 300
 Qy 301 QKVVLPDGVMSRPGSVLNLKLLITRARODDAGMYICLGANTMGYSFRSAPLTVLPDPK 360
 Db 301 QKVVLPDGVMSRPGSVLNLKLLITRARODDAGMYICLGANTMGYSFRSAPLTVLPDPK 360
 Qy 361 PPGPPVASSSSATSLPWPVIGIPAGAVFLLTLLMLCQAQKPCPTAPAPPLPGRPP 420
 Db 361 PPGPPVASSSSATSLPWPVIGIPAGAVFLLTLLMLCQAQKPCPTAPAPPLPGRPP 420
 Qy 421 GTARDSDGKDLPSLAALSAGPGVGLCEHSGSPAPOHLLGPGVAGPKLYPKLYTDIHT 480
 Db 421 GTARDSDGKDLPSLAALSAGPGVGLCEHSGSPAPOHLLGPGVAGPKLYPKLYTDIHT 480
 Qy 481 HTHSHSHSHVHGKVKHQHIHYQC 504
 Db 481 HTHSHSHSHVHGKVKHQHIHYQC 504

RESULT 8

ABU59072

The invention describes an isolated human PRO polypeptide. The PRO polypeptides are useful in detecting PRO polypeptides in a sample, in linking a bioactive molecule to a cell expressing a PRO polypeptide, and in modulating at least one biological activity of a cell expressing a PRO polypeptide. PRO131 stimulates hypertrophy of neonatal heart and is thus useful for treating cardiac insufficiency disorders. PRO1154 and PRO1186 stimulate adrenal cortical capillary endothelial growth, and PRO536.